

**CLAIMS**

1. A method of screening for and /or diagnosis of a cardiovascular disorder in a subject, comprising the steps of:
  - a) detecting and /or quantifying the level of a polypeptide in a biological sample from said subject, wherein the polypeptide is selected from:
    - i) a polypeptide comprising the amino acid sequence selected from the group consisting of: Cardiovascular disorder Plasma Polypeptides (CPPs) 30-148;
    - ii) a variant, with at least 75% sequence identity, having one or more amino acid substitutions, deletions or insertions relative to the amino acid sequence selected from the group consisting of: CPPs 30-148; and
    - iii) a fragment of a polypeptide as defined in i) or ii) above which is a least ten amino acids long; and
  - b) comparing said level to that of a control sample, wherein a decrease in said level relative to that of the control is indicative of a cardiovascular disorder.
2. A method of predicting a cardiovascular disorder in a subject, comprising the steps of:
  - a) detecting and /or quantifying the level of a polypeptide in a biological sample from said subject, wherein the polypeptide is selected from:
    - i) a polypeptide comprising the amino acid sequence selected from the group consisting of: Cardiovascular disorder Plasma Polypeptides (CPPs) 30-148;
    - ii) a variant, with at least 75% sequence identity, having one or more amino acid substitutions, deletions or insertions relative to the amino acid sequence selected from the group consisting of: CPPs 30-148; and
    - iii) a fragment of a polypeptide as defined in i) or ii) above which is a least ten amino acids long; and
  - b) comparing said level to that of a control sample, wherein a decrease in said level relative to that of the control indicates a risk of developing a cardiovascular disorder.
3. The method of claim 1 or 2, wherein said cardiovascular disorder is Coronary Artery Disease (CAD).
4. The method of any one of claims 1-3, wherein said biological sample is plasma.
5. The method of any one of claims 1-4, wherein said method is performed ex vivo.

6. The method of any one of claims 1-5, wherein said polypeptide is detected and /or quantified by mass spectrometry.
7. The method of any one of claims 1 to 5, wherein said polypeptide is detected and /or quantified by Enzyme-Linked Immuno Sorbent Assay.
8. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of Cardiovascular disorder Plasma Polypeptides (CPPs) 30-148, wherein said polypeptide is fused to a heterologous polypeptide sequence.
9. An anti-Cardiovascular disorder Plasma Polypeptide (CPP) antibody that selectively binds to a polypeptide comprising the amino acid sequence selected from the group consisting of CPPs 30-148.
10. A method of binding an antibody to a Cardiovascular disorder Plasma Polypeptide (CPP) comprising the steps of:
  - i) contacting the antibody of claim 8 with a biological sample under conditions that permit antibody binding; and
  - ii) removing contaminants.
11. The method of claim 10, wherein said antibody is attached to a label group.
12. The method of claim 10, wherein said sample is human plasma.
13. A method of identifying a Cardiovascular disorder Plasma Polypeptide (CPP) modulator comprising the steps of:
  - i) contacting a test compound with a polypeptide selected from the group consisting of CPPs 30-148 under sample conditions permissive for at least one CPP biological activity;
  - ii) determining the level of said at least one CPP biological activity;
  - iii) comparing said level to that of a control sample lacking said test compound; and
  - iv) selecting a test compound which causes said level to change for further testing as a CPP modulator for the prophylactic and/or therapeutic treatment of cardiovascular disorders.
14. An isolated polypeptide having the amino acid sequence of a Cardiovascular disorder Plasma Polypeptide (CPP) selected from the group of CPP 35, 39, 41, 60-62, 65-69, 71-72, 94-143,

- 15. An isolated polynucleotide encoding the polypeptide of claim 14.**
- 16. A method of identifying a modulator of a cardiovascular disorder comprising the steps of:**
- (a) administering a candidate agent to a non-human test animal which is predisposed to be affected or which is affected by the cardiovascular disorder;**
  - (b) administering the candidate agent of (a) to a matched control non-human animal not predisposed to be affected or not being affected by the cardiovascular disorder;**
  - (c) detecting and /or quantifying the level of a polypeptide in a biological sample obtained from the non-human test animal of step (a) and from the control animal of step (b), wherein the polypeptide is selected from:**
    - i) a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148);**
    - ii) a variant, with at least 75% sequence identity, having one or more amino acid substitutions, deletions or insertions relative to an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148); and**
    - iii) a fragment of a polypeptide as defined in i) or ii) above which is a least ten amino acids long; and**
  - (d) comparing the levels of the polypeptide of step (c); wherein a displacement of the level of the polypeptide in the biological sample obtained from the non-human test animal towards the level of the polypeptide in the biological sample obtained from the control animal indicates that the candidate agent is a modulator of the cardiovascular disorder.**
- 17. The method of claim 16, wherein the non-human test animal which is predisposed to be affected or which is affected by the cardiovascular disorder comprises a decreased plasma level of a polypeptide selected from:**
- i) a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148);**
  - ii) a variant, with at least 75% sequence identity, having one or more amino acid substitutions, deletions or insertions relative to an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148); and**
  - iii) a fragment of a polypeptide as defined in i) or ii) above which is a least ten amino acids long.**

**18. A method for monitoring the efficacy of a treatment of a subject having or at risk of developing a cardiovascular disorder with an agent, the method comprising:**

- (a) obtaining a pre-administration biological sample from the subject prior to administration of the agent;**
- (b) detecting and /or quantifying the level of a polypeptide in the biological sample from said subject, wherein the polypeptide is selected from:**
  - i) a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148);**
  - ii) a variant, with at least 75% sequence identity, having one or more amino acid substitutions, deletions or insertions relative to an amino acid sequence selected from the group consisting of the amino acid sequences listed in Table 3 (CPPs 30-148); and**
  - iii) a fragment of a polypeptide as defined in i) or ii) above which is a least ten amino acids long; and**
- (c) obtaining one or more post-administration biological samples from the subject;**
- (d) detecting the level of the polypeptide in the post-administration sample or samples;**
- (e) comparing the level of the polypeptide in the pre-administration sample with the level of the polypeptide in the post- administration sample; and**
- (f) adjusting the administration of the agent accordingly.**